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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/304,121

DATE: 08/16/1999
TIME: 16:44:06

Input Set: I304121.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED
AJ
PH#5
99

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1 <110> APPLICANT: Voellmy, Richard
2 <120> TITLE OF INVENTION: MOLECULAR REGULATORY CIRCUITS TO ACHIEVE
3   SUSTAINED ACTIVATION OF GENES OF INTEREST BY A SINGLE STRESS
4 <130> FILE REFERENCE: 870109.409
5 <140> CURRENT APPLICATION NUMBER: US/09/304,121
6 <141> CURRENT FILING DATE: 1999-05-03
7 <160> NUMBER OF SEQ ID NOS: 3
8 <170> SOFTWARE: FastSEQ for Windows Version 3.0
9 <210> SEQ ID NO 1
10 <211> LENGTH: 2156
11 <212> TYPE: DNA
12 <213> ORGANISM: Homo sapien
13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (161)...(1747)
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18   gggcgggcgc ggcccgaag gctggcgcg cgacggcggtt agcccgcccc tcggccccctc 120
19   tttgcggcgc ctccctcgc ctattccctc cttgctcgag atg gat ctg ccc gtg 175
20                                     Met Asp Leu Pro Val
21                                     1 5
22   ggc ccc ggc gcg gcg ggg ccc agc aac gtc ccg gcc ttc ctg acc aag 223
23   Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe Leu Thr Lys
24                                     10 15 20
25   ctg tgg acc ctc gtg agc gac ccg gac acc gac gcg ctc atc tgc tgg 271
26   Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu Ile Cys Trp
27                                     25 30 35
28   agc ccg agc ggg aac agc ttc cac gtg ttc gac cag ggc cag ttt gcc 319
29   Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly Gln Phe Ala
30                                     40 45 50
31   aag gag gtg ctg ccc aag tac ttc aag cac aac aac atg gcc agc ttc 367
32   Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met Ala Ser Phe
33                                     55 60 65
34   gtg cgg cag ctc aac atg tat ggc ttc cgg aaa gtg gtc cac atc gag 415
35   Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val His Ile Glu
36                                     70 75 80 85
37   cag ggc ggc ctg gtc aag cca gag aga gac gac acg gag ttc cag cac 463
38   Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp Thr Glu Phe Gln His
39                                     90 95 100
40   cca tgc ttc ctg cgt ggc cag gag cag ctc ctt gag aac atc aag agg 511
41   Pro Cys Phe Leu Arg Gly Gln Glu Gln Leu Leu Glu Asn Ile Lys Arg
42                                     105 110 115
43   aaa gtg acc agt gtg tcc acc ctg aag agt gaa gac ata aag atc cgc 559
44   Lys Val Thr Ser Val Ser Thr Leu Lys Ser Glu Asp Ile Lys Ile Arg

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45		120		125		130			
46	cag	gac	agc	gtc	acc	aag	ctg	ctg	acg
47	Gln	Asp	Ser	Val	Thr	Lys	Leu	Leu	Thr
48		135		140		145			
49	aag	cag	gag	tgc	atg	gac	tcc	aag	ctc
50	Lys	Gln	Glu	Cys	Met	Asp	Ser	Lys	Leu
51		150		155		160			
52	gag	gct	ctg	tgg	cgg	gag	gtg	gcc	agc
53	Glu	Ala	Leu	Trp	Arg	Glu	Val	Ala	Ser
54				170		175			
55	caa	cag	aaa	gtc	gtc	aac	aag	ctc	att
56	Gln	Gln	Lys	Val	Val	Asn	Lys	Leu	Ile
57				185		190			
58	cag	tca	aac	cgg	atc	ctg	ggg	gtg	aag
59	Gln	Ser	Asn	Arg	Ile	Leu	Gly	Val	Lys
60				200		205			
61	aac	gac	agt	ggc	tca	gca	cat	tcc	atg
62	Asn	Asp	Ser	Gly	Ser	Ala	His	Ser	Met
63				215		220			
64	tcc	ctg	gag	cac	gtc	cac	ggc	tcg	ggc
65	Ser	Leu	Glu	His	Val	His	Gly	Ser	Gly
66				230		235			
67	gcc	tac	agc	agc	tcc	agc	ctc	tac	gcc
68	Ala	Tyr	Ser	Ser	Ser	Ser	Leu	Tyr	Ala
69				250		255			
70	gga	ccc	atc	atc	tcc	gac	atc	acc	gag
71	Gly	Pro	Ile	Ile	Ser	Asp	Ile	Thr	Glu
72				265		270			
73	gcc	tcc	ccc	ggc	ggg	agc	ata	gac	gag
74	Ala	Ser	Pro	Gly	Gly	Ser	Ile	Asp	Glu
75				280		285			
76	ctg	gtg	cgt	gtc	aag	gag	gag	ccc	ccc
77	Leu	Val	Arg	Val	Lys	Glu	Glu	Pro	Pro
78				295		300			
79	gta	gag	gag	gcg	agt	ccc	ggg	cgc	cca
80	Val	Glu	Glu	Ala	Ser	Pro	Gly	Arg	Pro
81				310		315			
82	tcc	ccg	acc	gcc	ctc	att	gac	tcc	atc
83	Ser	Pro	Thr	Ala	Leu	Ile	Asp	Ser	Ile
84				330		335			
85	ccc	gcc	tcc	gtc	aca	gcc	ctc	acg	gac
86	Pro	Ala	Ser	Val	Thr	Ala	Leu	Thr	Asp
87				345		350			
88	gag	ggc	cgg	cct	ccc	tcc	ccc	ccg	ccc
89	Glu	Gly	Arg	Pro	Pro	Ser	Pro	Pro	Pro
90				360		365			
91	ctc	agc	gta	gcc	tgc	ctg	gac	aag	aat
92	Leu	Ser	Val	Ala	Cys	Leu	Asp	Lys	Asn
93				375		380			
94	gct	atg	gac	tcc	aac	ctg	gat	aac	ctg

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95      Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr Met Leu Ser Ser His
96      390                      395                      400                      405
97      ggc ttc agc gtg gac acc agt gcc ctg ctg gac ctg ttc agc ccc tcg      1423
98      Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp Leu Phe Ser Pro Ser
99                      410                      415                      420
100     gtg acc gtg ccc gac atg agc ctg cct gac ctt gac agc agc ctg gcc      1471
101     Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu Asp Ser Ser Leu Ala
102                      425                      430                      435
103     agt atc caa gag ctg tct ccc cag gag ccc ccc agg cct ccc gag      1519
104     Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg Pro Pro Glu
105                      440                      445                      450
106     gca gag aac agc agc ccg gat tca ggg aag cag ctg gtg cac tac aca      1567
107     Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln Leu Val His Tyr Thr
108                      455                      460                      465
109     gcg cag ccg ctg ttc ctg ctg gac ccc ggc tcc gtg gac acc ggg agc      1615
110     Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser Val Asp Thr Gly Ser
111     470                      475                      480                      485
112     aac gac ctg ccg gtg ctg ttt gag ctg gga gag ggc tcc tac ttc tcc      1663
113     Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu Gly Ser Tyr Phe Ser
114                      490                      495                      500
115     gaa ggg gac ggc ttc gcc gag gac ccc acc atc tcc ctg ctg aca ggc      1711
116     Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu Leu Thr Gly
117                      505                      510                      515
118     tcg gag cct ccc aaa gcc aag gac ccc act gtc tcc tagaggcccc      1757
119     Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val Ser
120                      520                      525
121     ggaggagctg ggccagccgc ccacccccac cccagtgca gggctgggtct tggggaggca      1817
122     gggcagcctc gcggtcttgg gcaactgggtg gtcggccgcc atagccccag taggacaaac      1877
123     gggctcgggt ctgggcagca cctctgggtca ggagggtcac cctggcctgc cagtctgcct      1937
124     tcccccaacc ccgtgtctctg tggtttggtt ggggcttcac agccacacct ggactgaccc      1997
125     tgcaggttgt tcatagtcag aattgtattt tggattttta cacaactgtc ccgttccccg      2057
126     ctccacagag atacacagat atatacacac agtggatgga cggacaagac aggcagagat      2117
127     ctataaacag acaggctcta aaaaaaaaaa aaaaaaaaaa      2156
128     <210> SEQ ID NO 2
129     <211> LENGTH: 529
130     <212> TYPE: PRT
131     <213> ORGANISM: Homo sapien
132     <400> SEQUENCE: 2
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135     Ala Phe Leu Thr Lys Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp
136     20                      25                      30
137     Ala Leu Ile Cys Trp Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp
138     35                      40                      45
139     Gln Gly Gln Phe Ala Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn
140     50                      55                      60
141     Asn Met Ala Ser Phe Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys
142     65                      70                      75                      80
143     Val Val His Ile Glu Gln Gly Gly Leu Val Lys Pro Glu Arg Asp Asp
144     85                      90                      95

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145	Thr	Glu	Phe	Gln	His	Pro	Cys	Phe	Leu	Arg	Gly	Gln	Glu	Gln	Leu	Leu
146				100					105					110		
147	Glu	Asn	Ile	Lys	Arg	Lys	Val	Thr	Ser	Val	Ser	Thr	Leu	Lys	Ser	Glu
148			115					120					125			
149	Asp	Ile	Lys	Ile	Arg	Gln	Asp	Ser	Val	Thr	Lys	Leu	Leu	Thr	Asp	Val
150		130					135					140				
151	Gln	Leu	Met	Lys	Gly	Lys	Gln	Glu	Cys	Met	Asp	Ser	Lys	Leu	Leu	Ala
152	145					150					155					160
153	Met	Lys	His	Glu	Asn	Glu	Ala	Leu	Trp	Arg	Glu	Val	Ala	Ser	Leu	Arg
154				165						170					175	
155	Gln	Lys	His	Ala	Gln	Gln	Gln	Lys	Val	Val	Asn	Lys	Leu	Ile	Gln	Phe
156			180						185					190		
157	Leu	Ile	Ser	Leu	Val	Gln	Ser	Asn	Arg	Ile	Leu	Gly	Val	Lys	Arg	Lys
158		195					200					205				
159	Ile	Pro	Leu	Met	Leu	Asn	Asp	Ser	Gly	Ser	Ala	His	Ser	Met	Pro	Lys
160		210					215				220					
161	Tyr	Ser	Arg	Gln	Phe	Ser	Leu	Glu	His	Val	His	Gly	Ser	Gly	Pro	Tyr
162	225					230					235					240
163	Ser	Ala	Pro	Ser	Pro	Ala	Tyr	Ser	Ser	Ser	Ser	Leu	Tyr	Ala	Pro	Asp
164				245					250						255	
165	Ala	Val	Ala	Ser	Ser	Gly	Pro	Ile	Ile	Ser	Asp	Ile	Thr	Glu	Leu	Ala
166			260						265					270		
167	Pro	Ala	Ser	Pro	Met	Ala	Ser	Pro	Gly	Gly	Ser	Ile	Asp	Glu	Arg	Pro
168		275					280					285				
169	Leu	Ser	Ser	Ser	Pro	Leu	Val	Arg	Val	Lys	Glu	Glu	Pro	Pro	Ser	Pro
170		290				295					300					
171	Pro	Gln	Ser	Pro	Arg	Val	Glu	Glu	Ala	Ser	Pro	Gly	Arg	Pro	Ser	Ser
172	305				310						315					320
173	Val	Asp	Thr	Leu	Leu	Ser	Pro	Thr	Ala	Leu	Ile	Asp	Ser	Ile	Leu	Arg
174				325					330					335		
175	Glu	Ser	Glu	Pro	Ala	Pro	Ala	Ser	Val	Thr	Ala	Leu	Thr	Asp	Ala	Arg
176			340						345					350		
177	Gly	His	Thr	Asp	Thr	Glu	Gly	Arg	Pro	Pro	Ser	Pro	Pro	Pro	Thr	Ser
178		355					360					365				
179	Thr	Pro	Glu	Lys	Cys	Leu	Ser	Val	Ala	Cys	Leu	Asp	Lys	Asn	Glu	Leu
180		370				375					380					
181	Ser	Asp	His	Leu	Asp	Ala	Met	Asp	Ser	Asn	Leu	Asp	Asn	Leu	Gln	Thr
182	385				390					395						400
183	Met	Leu	Ser	Ser	His	Gly	Phe	Ser	Val	Asp	Thr	Ser	Ala	Leu	Leu	Asp
184				405					410					415		
185	Leu	Phe	Ser	Pro	Ser	Val	Thr	Val	Pro	Asp	Met	Ser	Leu	Pro	Asp	Leu
186			420						425				430			
187	Asp	Ser	Ser	Leu	Ala	Ser	Ile	Gln	Glu	Leu	Leu	Ser	Pro	Gln	Glu	Pro
188		435					440					445				
189	Pro	Arg	Pro	Pro	Glu	Ala	Glu	Asn	Ser	Ser	Pro	Asp	Ser	Gly	Lys	Gln
190		450				455					460					
191	Leu	Val	His	Tyr	Thr	Ala	Gln	Pro	Leu	Phe	Leu	Leu	Asp	Pro	Gly	Ser
192	465				470					475						480
193	Val	Asp	Thr	Gly	Ser	Asn	Asp	Leu	Pro	Val	Leu	Phe	Glu	Leu	Gly	Glu
194				485					490					495		

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195 Gly Ser Tyr Phe Ser Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile
196 500 505 510
197 Ser Leu Leu Thr Gly Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val
198 515 520 525
199 Ser
200 <210> SEQ ID NO 3
201 <211> LENGTH: 25
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: A heat shock element. A nucleic acid molecule
206 that binds with a heat shock transcription factor
207 to stimulate gene expression
208 <220> FEATURE:
209 <221> NAME/KEY: misc_feature
210 <222> LOCATION: (1)...(25).
211 <223> OTHER INFORMATION: n = A,T,C or G
212 <400> SEQUENCE: 3
W--> 213 ngaannttcn nnnnnnttcn ngaan

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text

213 W "N" or "Xaa" used: Feature required

ngaannttcn nnnnnnttcn ngan